



1/12

Compd #	MOLSTRUCTURE
---------	--------------

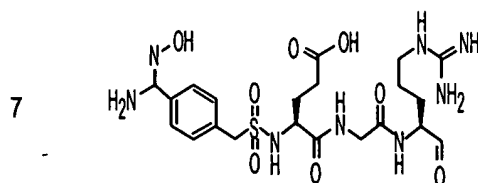
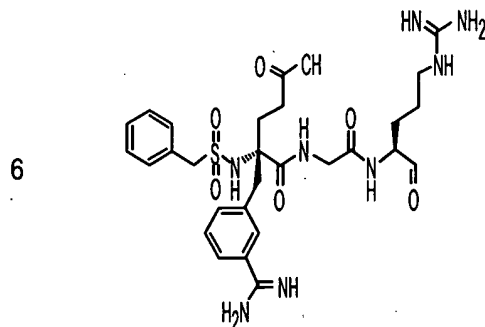
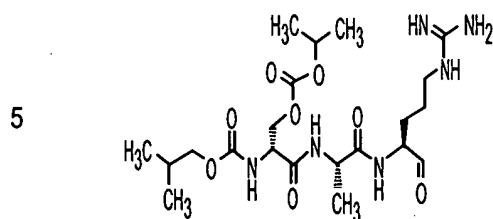
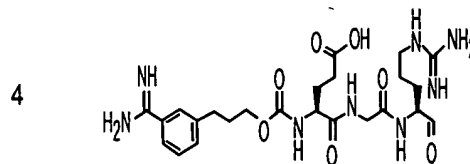
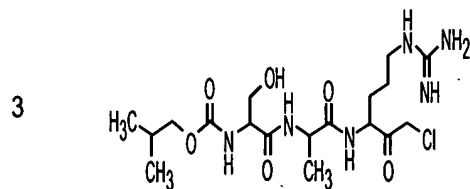
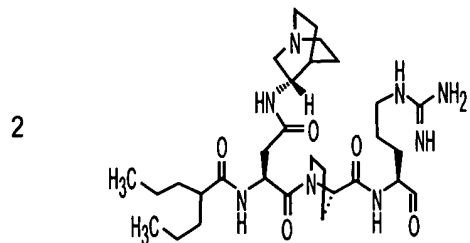
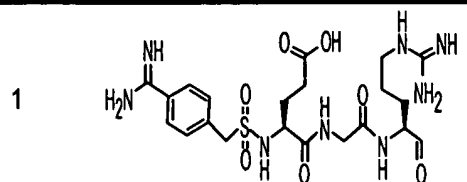


FIG. 1A

2/12

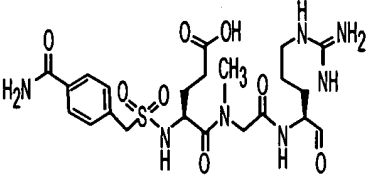
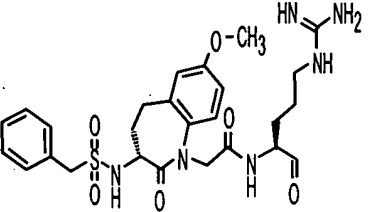
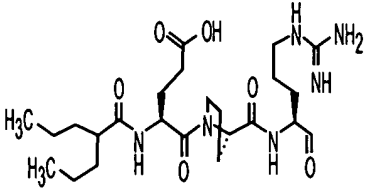
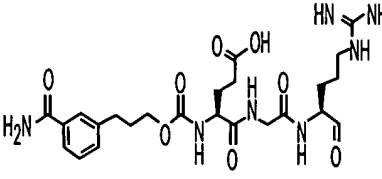
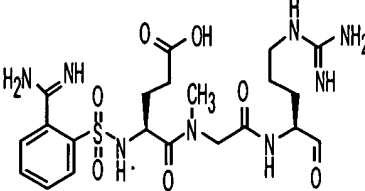
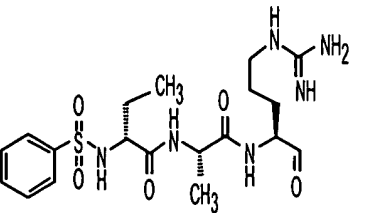
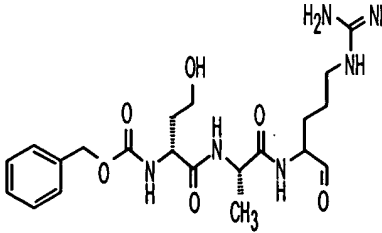
Compd #	MOLSTRUCTURE
8	
9	
10	
11	
12	
13	
14	

FIG. 1B

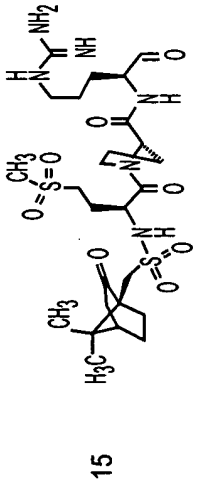
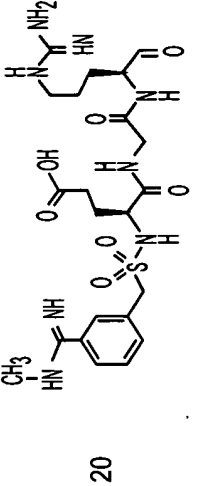
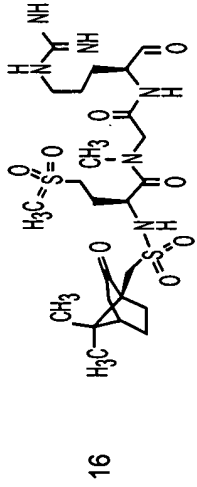
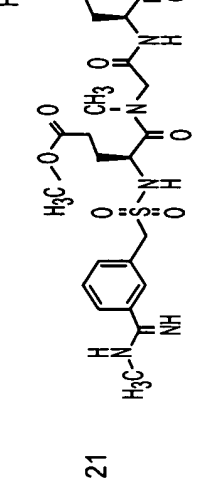
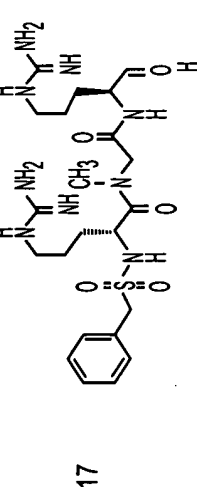
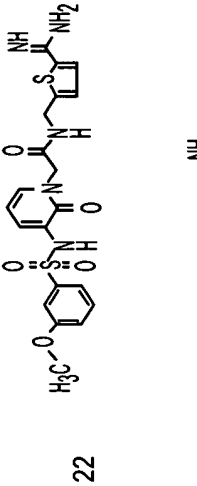
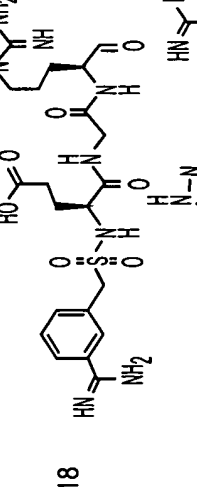
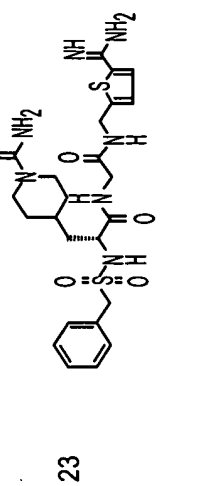
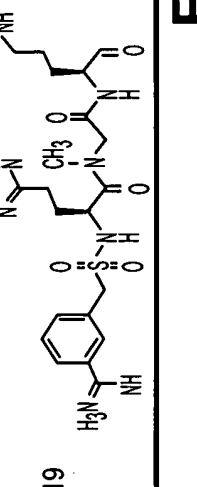
Compd #	MOLSTRUCTURE	Compd #	MOLSTRUCTURE
15		20	
16		21	
17		22	
18		23	
19			

FIG. 1C

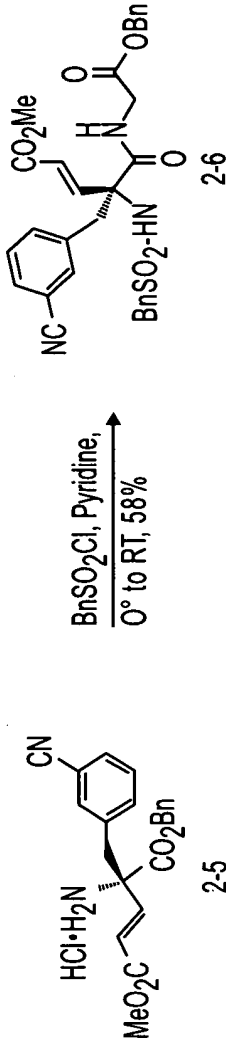
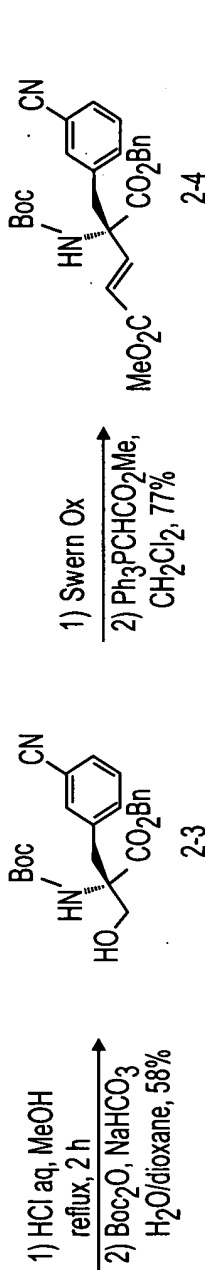
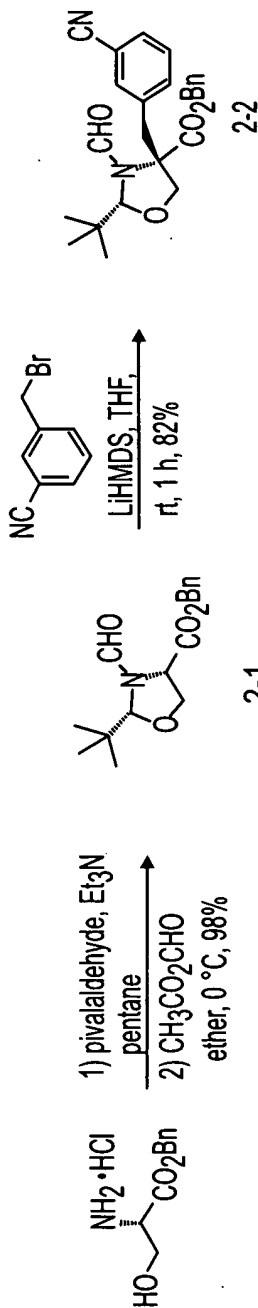


FIG. 2A

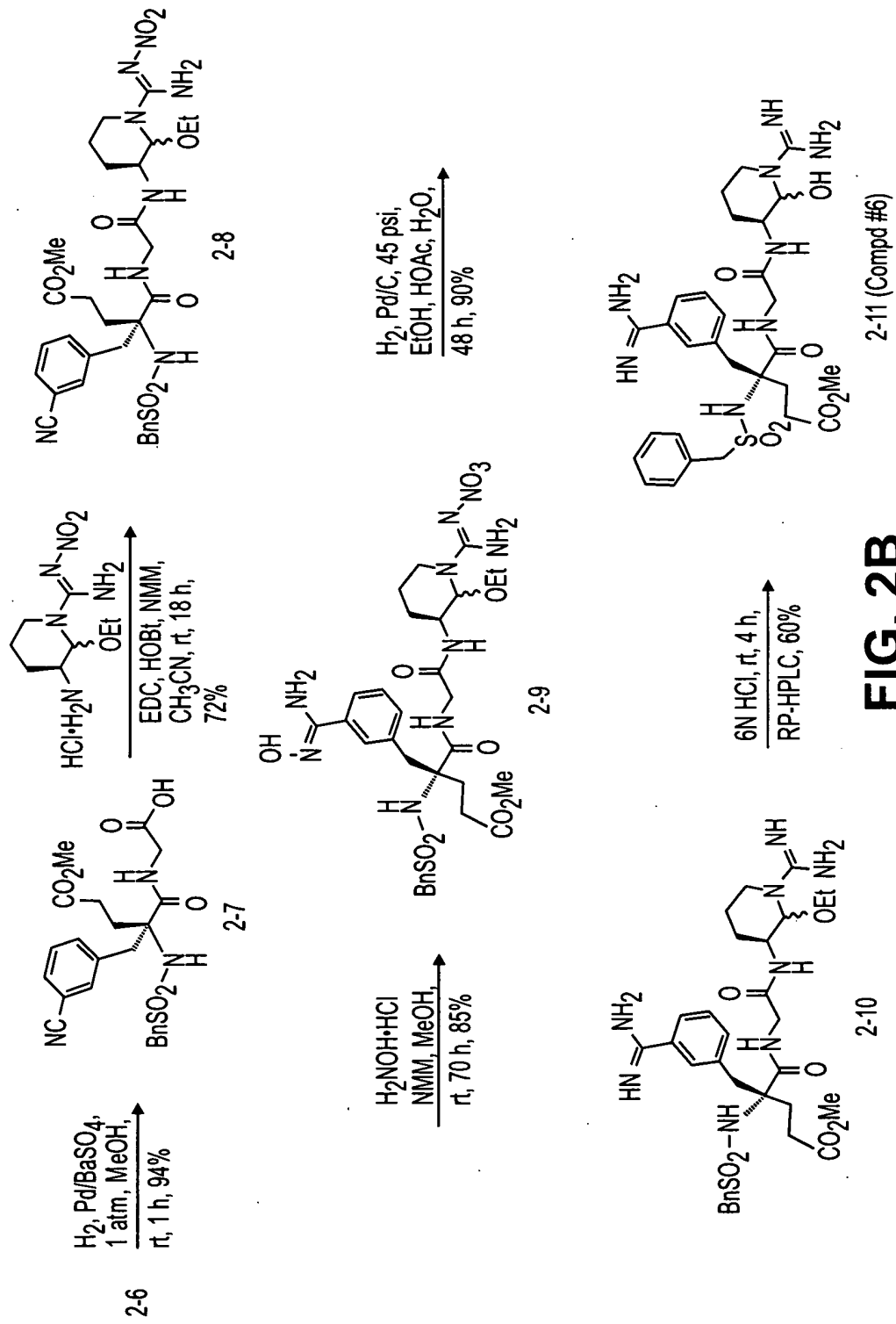


FIG. 2B

6/12

```

      10      20      30      40      50      60
GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT
CAACAACCCCCGTGCCTACGCCTACTCCCGCTCACCGGGACCGTCCATTTCGGACGTACGA
  V  V  G  G  T  D  A  D  E  G  E  H  P  W  Q  V  S  L  H  A>
      70      80      90     100     110     120
CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC
GACCCGGTCCCGGTGTAGACGCCACGAAGGGAGTAGAGAGGGTTGACCGACCAGAGACGG
  L  G  Q  G  H  I  C  G  A  S  L  I  S  P  N  W  L  V  S  A>
      130     140     150     160     170     180
GCACACTGCTACATCGATGACAGAGGATTTCAGGTACTCAGACCCACGCAGTGGACGGCC
CGTGTGACGATGTAGCTACTGTCTCCTAAGTCCATGAGTCTGGGGTGCGTACCTGCCGG
  A  H  C  Y  I  D  D  R  G  F  R  Y  S  D  P  T  Q  W  T  A>
      190     200     210     220     230     240
TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC
AAGGACCCGAACGTGCTGGTCTCGGTTCGCGTCGCGGGGACCCACGTCCTCGCGTCCGAG
  F  L  G  L  H  D  Q  S  Q  R  S  A  P  G  V  Q  E  R  R  L>
      250     260     270     280     290     300
AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG
TTCGCGTAGTAGAGGGTGGGGAAGAAGTTACTGAAGTGGAAGCTGATACTGTAGCGCGAC
  K  R  I  I  S  H  P  F  F  N  D  F  T  F  D  Y  D  I  A  L>
      310     320     330     340     350     360
CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC
GACCTCGACCTCTTTGGCCGTCTCATGTCGAGGTACCACGCCGGGTAGACGGACGGCCTG
  L  E  L  E  K  P  A  E  Y  S  S  M  V  R  P  I  C  L  P  D>

```

FIG. 3A

7/12

```

      370      380      390      400      410      420
GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTACGGGCTGGGGACACACCCAG
CGGAGGGTACAGAAGGGACGGCCGTTCCGGTAGACCCAGTGCCCGACCCCTGTGTGGGTC
  A  S  H  V  F  P  A  G  K  A  I  W  V  T  G  W  G  H  T  Q>

      430      440      450      460      470      480
TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC
ATACCTCCGTGACCGCGCGACTAGGACGTTTTCCCACTCTAGGCGCAGTAGTTGGTCTGG
  Y  G  G  T  G  A  L  I  L  Q  K  G  E  I  R  V  I  N  Q  T>

      490      500      510      520      530      540
ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC
TGGACGCTCTTGGAGGACGGCGTCGTCTAGTGCGGCGCGTACTACACGCACCCGAAGGAG
  T  C  E  N  L  L  P  Q  Q  I  T  P  R  M  M  C  V  G  F  L>

      550      560      570      580      590      600
AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG
TCGCCGCCGCACCTGAGGACGGTCCCACTAAGGCCCCCTGGGGACAGGTTCGCACCTCCGC
  S  G  G  V  D  S  C  Q  G  D  S  G  G  P  L  S  S  V  E  A>

      610      620      630      640      650      660
GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC
CTACCCGCCTAGAAGGTCCGGCCACACCACTCGACCCCTCTGCCGACGCGAGTCTCCTTG
  D  G  R  I  F  Q  A  G  V  V  S  W  G  D  G  C  A  Q  R  N>

      670      680      690      700      710      720
AAGCCAGGCGTGACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACTGGG
TTCGGTCCGCACATGTGTTCCGAGGGAGACAAAGCCCTGACCTAGTTTCTCTTGACCC
  K  P  G  V  Y  T  R  L  P  L  F  R  D  W  I  K  E  N  T  G>

```

FIG. 3B

8/12

GTATAG

CATATC

V *>

FIG. 3C

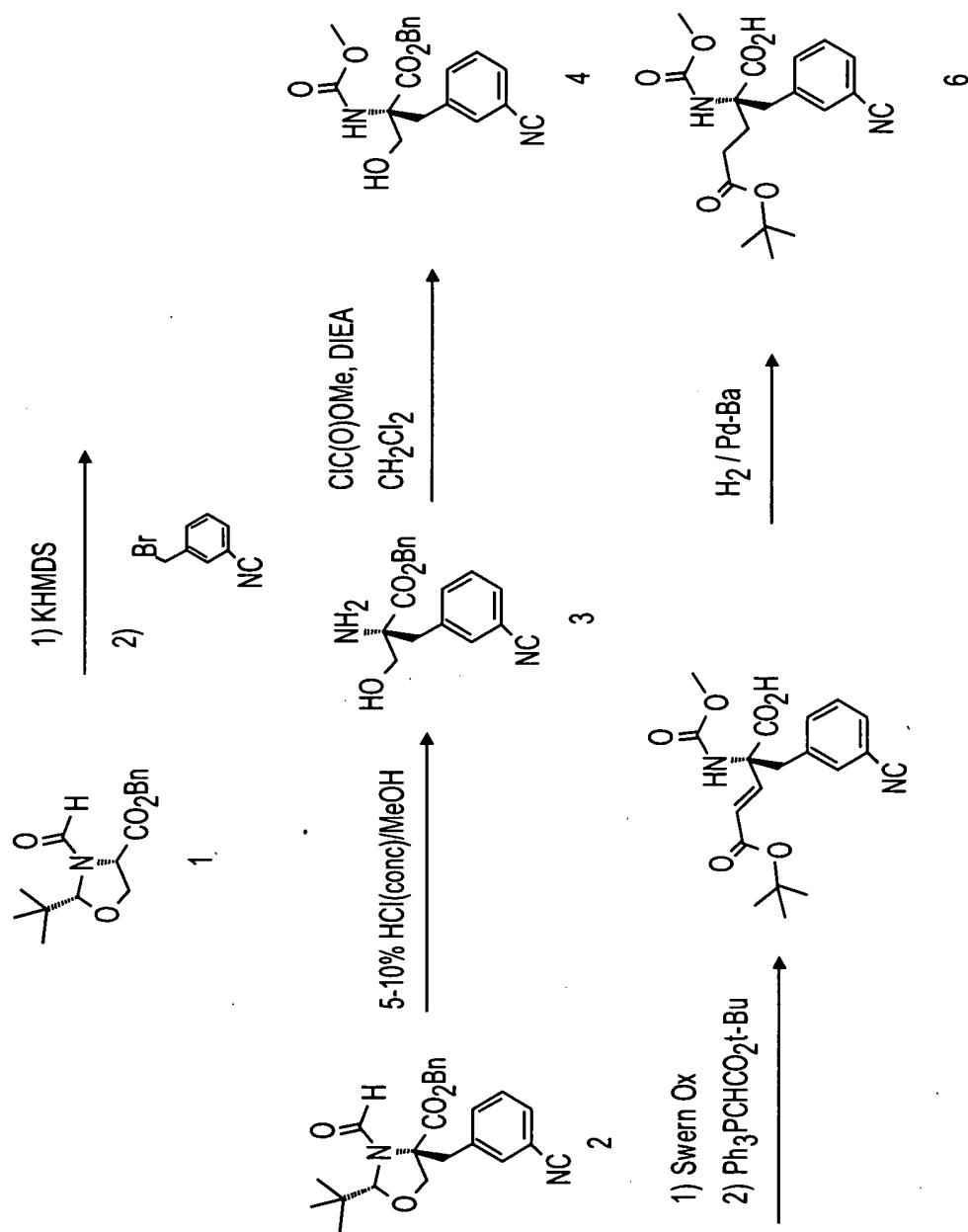


FIG. 4A

10/12

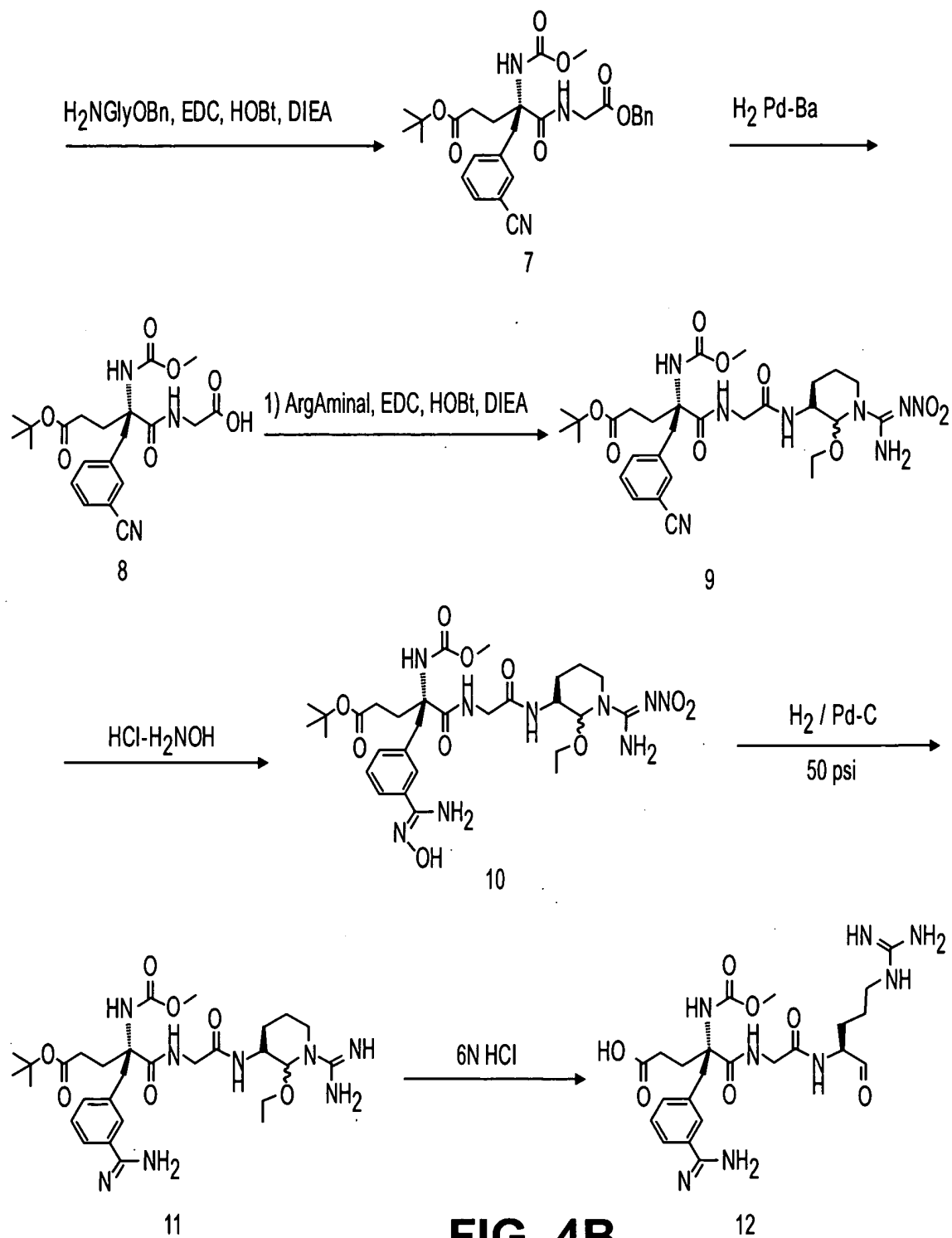


FIG. 4B

REPLACEMENT SHEET

11/12

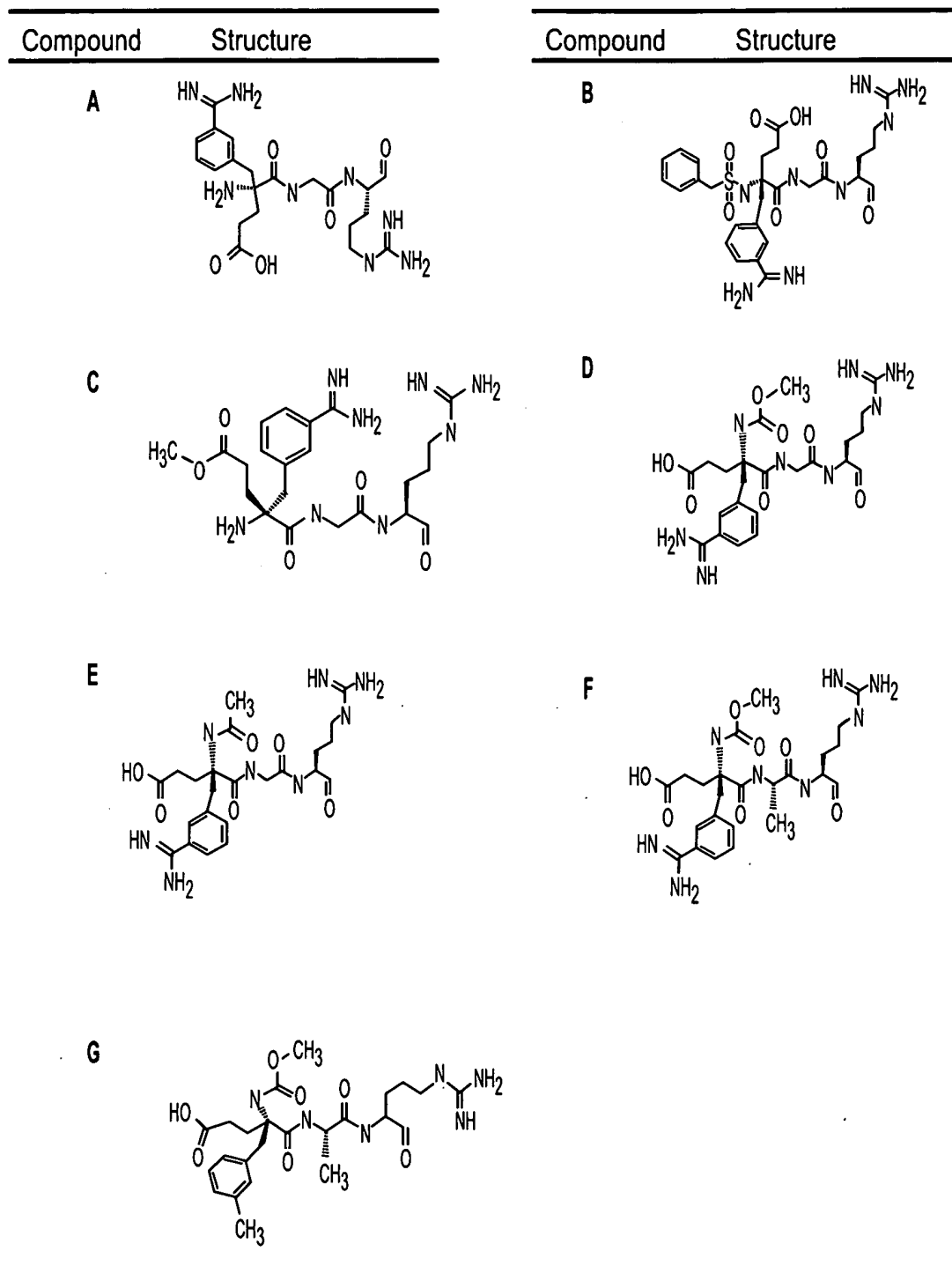


FIG. 5A

Compound	Structure	Compound	Structure
H		I	
J		K	
L		M	

FIG. 5B